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DATE: Friday, November 12, 2004

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☐	L5	L4 and crystal$6	5
☐	L4	(udp adj3 glycosyl adj3 transferase or murg) same coli	23
☐	L3	udp adj3 glycosyl adj3 transferase same coli	2
☐	L2	udp-glycosyltransferase same coli	0
☐	L1	udp-glycosyltransferase same coli and crystal	0

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☐ 1. Document ID: US 6737237 B1

Using default format because multiple data bases are involved.

L3: Entry 1 of 2 File: USPT May 18, 2004

US-PAT-NO: 6737237
DOCUMENT-IDENTIFIER: US 6737237 B1

TITLE: Antimicrobial agents, diagnostic reagents, and vaccines based on unique Apicomplexan parasite components

DATE-ISSUED: May 18, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
McLeod; Rima L.	Chicago	IL		
Roberts; Craig W.	Glasgow			GB
Roberts; Fiona	Glasgow			GB
Johnson; Jennifer J.	Stillwater	MN		
Kirisits; Michael	Chicago	IL		
Ferguson; David	Tackley Oxford			GB
Lyons; Russell	Glasgow			GB
Mui; Ernest	Chicago	IL		
Mack; Doug	Riverside	IL		
Samuel; Benjamin	Chicago	IL		
Gornicki; Piotr	Chicago	IL		
Zuther; Ellen	Beuhy			DE

US-CL-CURRENT: 435/6; 435/19, 435/254.2, 435/320.1, 435/69.1, 435/7.2, 435/7.22, 536/23.7, 536/23.74

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

☐ 2. Document ID: US 6699654 B1

L3: Entry 2 of 2 File: USPT Mar 2, 2004

US-PAT-NO: 6699654
DOCUMENT-IDENTIFIER: US 6699654 B1

TITLE: Antimicrobial agents diagnostic reagents, and vaccines based on unique apicomplexan parasite components

DATE-ISSUED: March 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
McLeod; Rima L. W.	Chicago	IL	60637	
Roberts; Craig W.	Kirklee, Glasgow, G12 OTW Scotland			GB
Roberts; Fiona	Kirklee, Glasgow, G12 OTW Scotland			GB
Johnson; Jennifer J.	Bolingbrook	IL	60440	
Mets; Laurens	Wilmette	IL	60091	

US-CL-CURRENT: 435/4; 435/6, 435/7.1

ABSTRACT:

This invention relates uses of components of plant-like metabolic pathways not including psbA or PPi phosphofructokinase and not generally operative in animals or encoded by the plastid DNA, to develop compositions that interfere with Apicomplexan growth and survival. Components of the pathways include enzymes, transit peptides and nucleotide sequences encoding the enzymes and peptides, or promoters of these nucleotide sequences to which antibodies, antisense molecules and other inhibitors are directed. Diagnostic and therapeutic reagents and vaccines are developed based on the components and their inhibitors.

9 Claims, 20 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 16

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Search Results - Record(s) 1 through 5 of 5 returned.

☐ 1. Document ID: US 6737237 B1

Using default format because multiple data bases are involved.

L5: Entry 1 of 5 File: USPT May 18, 2004

US-PAT-NO: 6737237
DOCUMENT-IDENTIFIER: US 6737237 B1

TITLE: Antimicrobial agents, diagnostic reagents, and vaccines based on unique Apicomplexan parasite components

DATE-ISSUED: May 18, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
McLeod; Rima L.	Chicago	IL		
Roberts; Craig W.	Glasgow			GB
Roberts; Fiona	Glasgow			GB
Johnson; Jennifer J.	Stillwater	MN		
Kirisits; Michael	Chicago	IL		
Ferguson; David	Tackley Oxford			GB
Lyons; Russell	Glasgow			GB
Mui; Ernest	Chicago	IL		
Mack; Doug	Riverside	IL		
Samuel; Benjamin	Chicago	IL		
Gornicki; Piotr	Chicago	IL		
Zuther; Ellen	Beuhy			DE

US-CL-CURRENT: 435/6; 435/19, 435/254.2, 435/320.1, 435/69.1, 435/7.2, 435/7.22, 536/23.7, 536/23.74

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw De

☐ 2. Document ID: US 6699654 B1

L5: Entry 2 of 5 File: USPT Mar 2, 2004

US-PAT-NO: 6699654
DOCUMENT-IDENTIFIER: US 6699654 B1

TITLE: Antimicrobial agents diagnostic reagents, and vaccines based on unique apicomplexan parasite components

DATE-ISSUED: March 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
McLeod; Rima L. W.	Chicago	IL	60637	
Roberts; Craig W.	Kirklee, Glasgow, G12 OTW Scotland			GB
Roberts; Fiona	Kirklee, Glasgow, G12 OTW Scotland			GB
Johnson; Jennifer J.	Bolingbrook	IL	60440	
Mets; Laurens	Wilmette	IL	60091	

US-CL-CURRENT: 435/4; 435/6, 435/7.1

ABSTRACT:

This invention relates uses of components of plant-like metabolic pathways not including psbA or PPi phosphofructokinase and not generally operative in animals or encoded by the plastid DNA, to develop compositions that interfere with Apicomplexan growth and survival. Components of the pathways include enzymes, transit peptides and nucleotide sequences encoding the enzymes and peptides, or promoters of these nucleotide sequences to which antibodies, antisense molecules and other inhibitors are directed. Diagnostic and therapeutic reagents and vaccines are developed based on the components and their inhibitors.

9 Claims, 20 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 16

☐ 3. Document ID: US 6583275 B1

L5: Entry 3 of 5 File: USPT Jun 24, 2003

US-PAT-NO: 6583275
DOCUMENT-IDENTIFIER: US 6583275 B1

TITLE: Nucleic acid sequences and expression system relating to Enterococcus faecium for diagnostics and therapeutics

DATE-ISSUED: June 24, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Doucette-Stamm; Lynn A.	Framingham	MA		
Bush; David	Somerville	MA		

US-CL-CURRENT: 536/23.1; 435/243, 435/320.1, 435/325, 435/6, 536/24.3, 536/24.32

ABSTRACT:

The invention provides isolated polypeptide and nucleic acid sequences derived Enterococcus faecium that are useful in diagnosis and therapy of pathological

conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

34 Claims, 0 Drawing figures
Exemplary Claim Number: 1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 4. Document ID: US 6356845 B1

L5: Entry 4 of 5 File: USPT Mar 12, 2002

US-PAT-NO: 6356845
DOCUMENT-IDENTIFIER: US 6356845 B1

TITLE: Crystallization and structure determination of Staphylococcus aureus UDP-N-acetylenolpyruvylglucosamine reductase (S. aureus MurB)

DATE-ISSUED: March 12, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Benson; Timothy E.	Kalamazoo	MI		
Harris; Melissa S.	Marshall	MI		

US-CL-CURRENT: 702/19; 435/183, 702/27

ABSTRACT:

The substrate free form of Staphylococcus aureus UDP-N-acetylenolpyruvylglucosamine reductase (S. aureus MurB) has been crystallized, and the three dimensional x-ray crystal structure has been solved to 2.3 .ANG. resolution. The x-ray crystal structure is useful for solving the structure of other molecules or molecular complexes, and designing inhibitors of S. aureus MurB.

7 Claims, 628 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 625

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. D

☐ 5. Document ID: US 20030077803 A1, WO 200190301 A2, AU 200151467 A

L5: Entry 5 of 5 File: DWPI Apr 24, 2003

DERWENT-ACC-NO: 2002-171402
DERWENT-WEEK: 200330

TITLE: Novel composition comprising crystalline form of MurG protein, a membrane-associated UDP-glycosyltransferase involved in peptidoglycan biosynthesis, for determining ability of chemical compound to bind MurG protein

INVENTOR: HA, S; WALKER, S

PRIORITY-DATA: 2000US-204930P (May 17, 2000), 2001US-0829275 (April 9, 2001)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 20030077803 A1	April 24, 2003		000	C12N009/22
WO 200190301 A2	November 29, 2001	E	222	C12N000/00
AU 200151467 A	December 3, 2001		000	C12N000/00

INT-CL (IPC): C12 N 0/00; C12 N 9/22; G01 N 33/48; G01 N 33/50; G06 F 19/00

ABSTRACTED-PUB-NO: WO 200190301A
BASIC-ABSTRACT:

NOVELTY - A composition (I) comprising a MurG, preferably Escherichia coli protein in crystalline form, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a three-dimensional (3D) structure of the crystalline form of a MurG protein, preferably E. coli MurG protein, where the 3D structure conforms to the atomic coordinates given in the specification;

(2) a 3D structure (IV) of the alpha -carbon backbone of the crystalline form of an E. coli MurG protein, where the 3D structure conforms to the atomic coordinates given in the specification;

(3) a 3D structure (V) of the alpha -carbon backbone and conserved amino acid residues of an E. coli MurG protein, where the 3D structure conforms to the atomic coordinates given in the specification;

(4) 3D structure (VI) of a donor nucleotide binding site of a MurG protein, where the 3D structure of the binding site conforms to the atomic coordinates given in the specification;

(5) a 3D structure (VII) of an acceptor binding site of a MurG protein substantially conforming to the atomic coordinates given in the specification;

(6) a 3D structure (VIII) of a membrane association site of a MurG protein substantially conforming to the atomic coordinates given in the specification;

(7) a 3D computer image (IX) of (IV), (V), (VI), (VII) or (VIII);

(8) a computer readable medium (X) encoded with a set of 3D coordinates of a MurG protein, alpha -carbon backbone of a MurG protein, an alpha -carbon backbone and conserved amino acid residues of a MurG protein, a donor nucleotide binding site of a MurG protein, an acceptor binding site of a MurG protein, or a membrane association site of a MurG protein, where using a graphical display software program, the 3D coordinates create an electronic file that can be visualized on a computer capable of representing the electronic file as a 3D image;

(9) identifying (M1) a potential inhibitor of a UDP-glycosyltransferase enzyme, comprising:

(a) using a 3D structure of UDP-glycosyltransferase enzyme as defined by atomic coordinates of UDP-glycosyltransferase enzyme;

(b) employing the 3D structure to design or select the potential inhibitor;

(c) synthesizing the potential inhibitor; and

(d) contacting the potential inhibitor with the UDP-glycosyltransferase enzyme in the presence of a substrate to test the ability of the potential inhibitor to inhibit the UDP-glycosyltransferase enzyme;

(10) a model (XI) of UDP-glycosyltransferase, a donor nucleotide binding site of a UDP-glycosyltransferase (MurG) protein, an acceptor binding site of MurG protein, or membrane association site of MurG protein, where the model represents a 3D structure that conforms to the atomic coordinates given in the specification;

(11) a model (XII) of the 3D structure of a MurG protein, produced by:

(a) providing an amino acid sequence of a MurG protein an E. coli MurG protein;

(b) identifying structurally conserved regions shared between the MurG protein and the E. coli MurG protein; and

(c) determining atomic coordinates for the MurG protein by assigning the structurally conserved regions of the MurG protein to 3D structure using a 3D structure of the MurG protein which substantially conforms to the atomic coordinates given in the specification, to derive a model of the 3D structure of the MurG amino acid sequence;

(12) determining (M2) a 3D structure of a MurG protein, comprising:

(a) providing an amino acid sequence of a MurG protein, where the 3D structure of the MurG protein is not known;

(b) analyzing the pattern of folding of the amino acid sequence in a 3D conformation by fold recognition; and

(c) comparing the pattern of folding of the MurG protein amino acid sequence with the 3D structure of the E. coli MurG protein, where the 3D structure of the E. coli MurG protein conforms to the atomic coordinates given in the specification;

(13) deriving (M3) a model of 3D structure of a MurG protein, comprising:

(a) providing an amino acid sequence of a MurG protein;

(b) identifying structurally conserved regions shared between the MurG protein and the E. coli MurG protein; and

(c) determining atomic coordinates for the MurG protein structure by assigning the structurally conserved regions of the MurG protein to a 3D structure of the E. coli MurG protein based on atomic coordinates given in the specification to derive a model of the 3D structure of the MurG protein amino acid sequence; and

(14) deriving (M4) a 3D structure of a crystallized MurG protein, comprising:

(a) comparing the Patterson function of a crystallized MurG protein with the Patterson function of crystalline E. coli MurG protein to produce an electron-density map of the crystallized MurG protein; and

(b) analyzing the electron-density map to produce the 3D structure of the crystallized MurG protein.

ACTIVITY - Antibiotic; antimicrobial.

No biological data is given.

MECHANISM OF ACTION - Modulator of glycosyltransferase activity (claimed).

USE - (IX) is useful to design a compound. (XI) is useful in a computer-assisted method of structure based drug design of bioactive compounds, by providing (XI) and designing a chemical compound using (XI). The method further comprises synthesizing the chemical compound, and evaluating the bioactivity of the synthesized chemical compound. The bioactivity is selected from inhibiting binding of a nucleotide donor compound or an acceptor compound to the MurG protein, or inhibiting association of the MurG protein to a membrane. Designing the chemical compound involves computational screening of one or more database of chemical compounds in which the 3D structure of the compounds are known, and interacting a compound identified by the screening step with the model by computer. The step of designing involves directed drug design, random drug design, or grid-based drug design. Designing involves selecting compounds which are predicted to bind to or mimic the 3D structure of the MurG protein. (All claimed). (IV), (V), (VI), (VII), (VIII), (XI) or (XII) is useful to derive other MurG structures and in ligand discovery and drug discovery strategies. A modulator of glycosyltransferase is useful as antibiotics or antimicrobial agents in animals, and therapeutically or diagnostically in an animal.

Terms	Documents
L4 and crystal$6	5